Fig. 1

Fig. 2

ApaLI (6020)
Amp
CMV
NcoI (611)
PmeI (905)
HindIII (912)
BamHI (930)
EcoRI (953)
XbaI (1026)
XbaI (1152)
BamHI (1290)
bolinopsin
HindIII (1640)
EcoRV (1667)
XbaI (1823)
XhoI (1829)
AvaI (1829)
XbaI (1835)
PmeI (1850)
PolyA
ApaLI (4774)
pcDNA3-bolinopsin
6275 bp
NcoI (3541)
Neo
PstI (3162)
NcoI (2806)
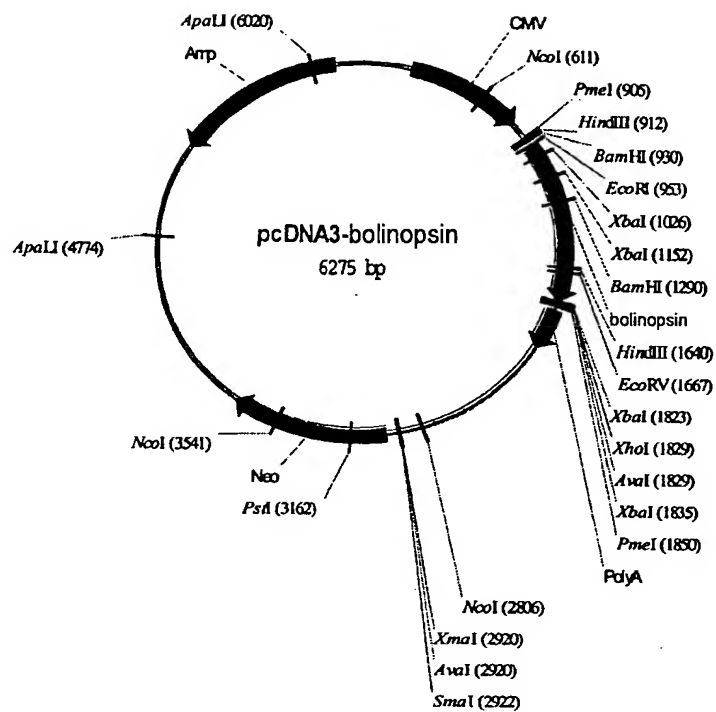XmaI (2920)
AvaI (2920)
SmaI (2922)
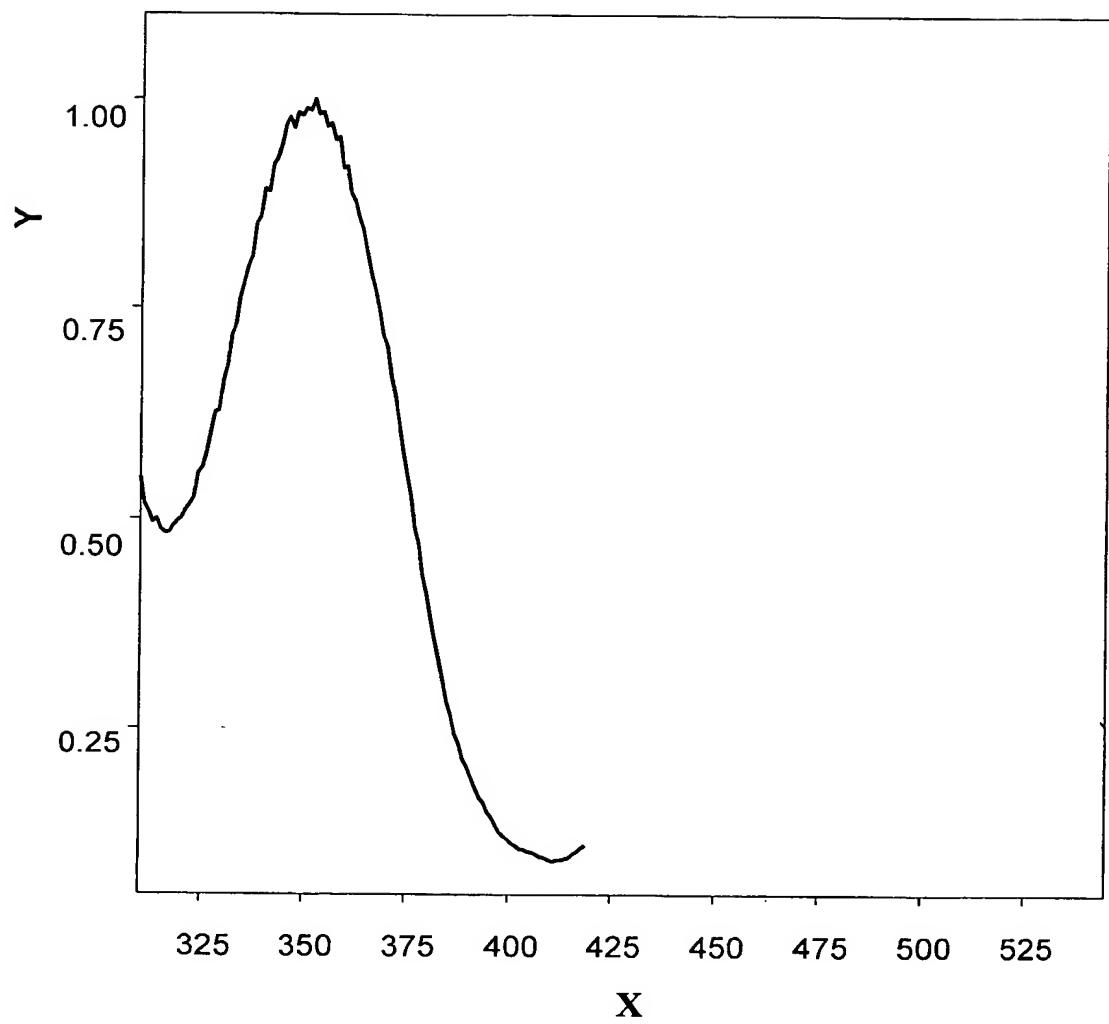
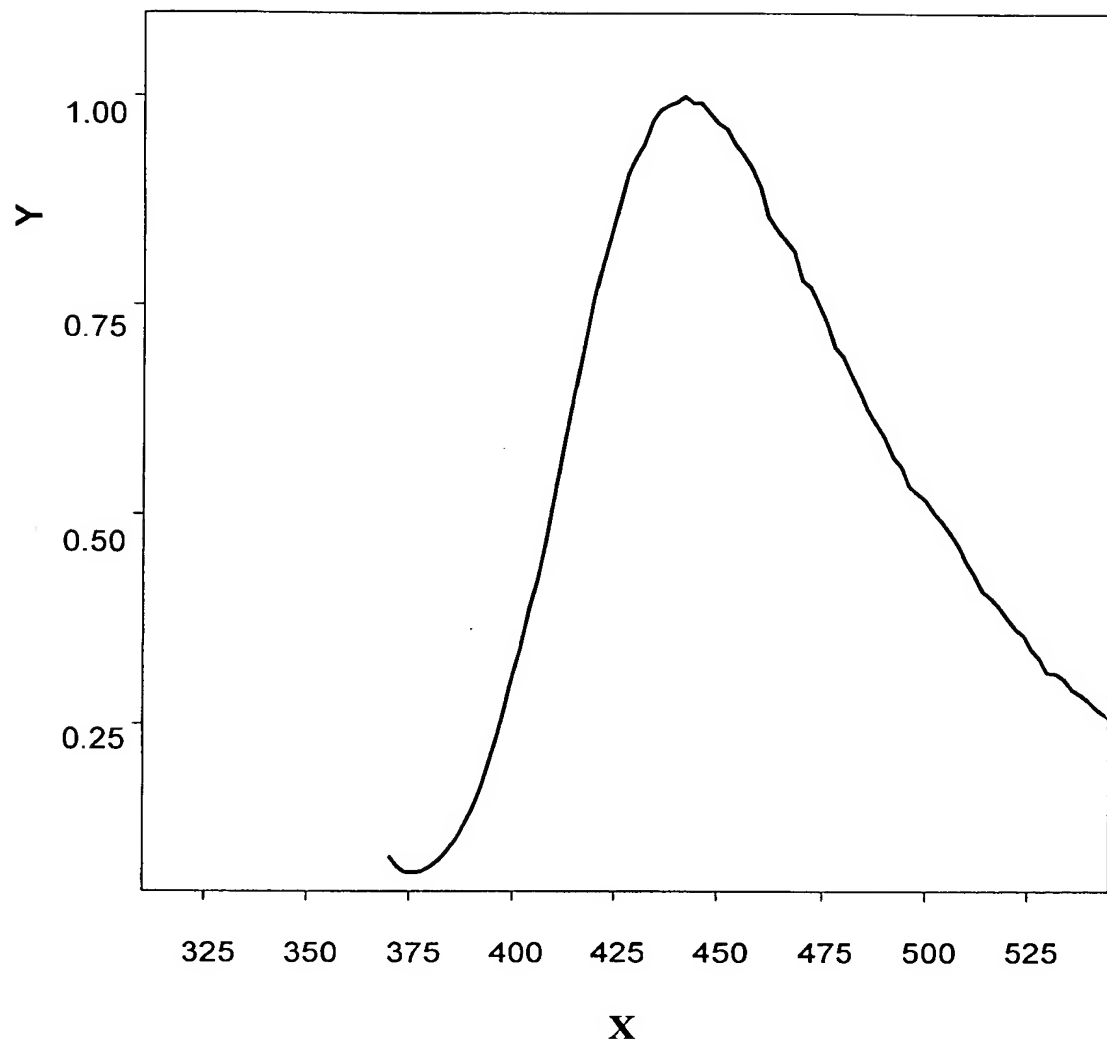**Fig. 3**

Fig. 4

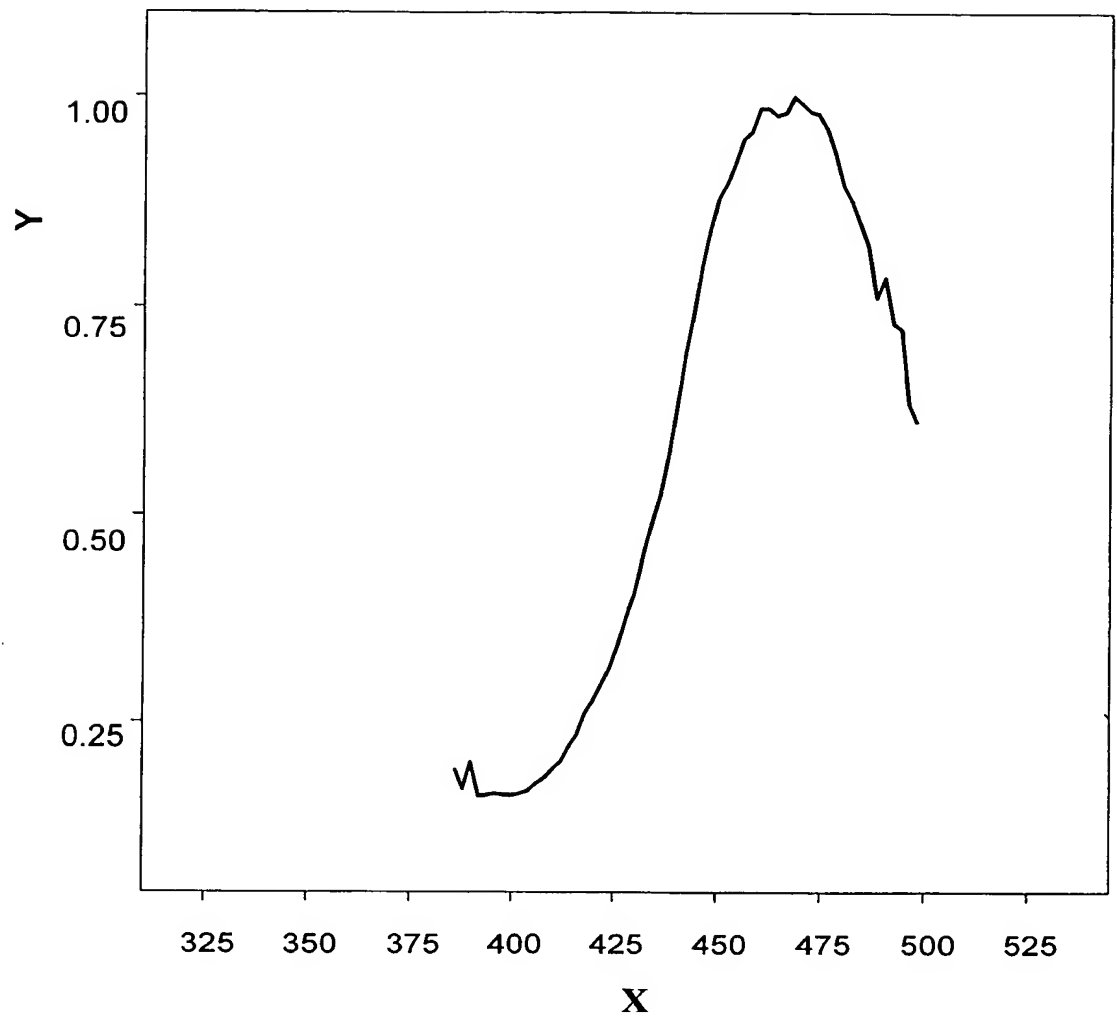**Fig. 5**

Fig. 6

```
aequorin   _000:ATGACAAGCAAACAATACTCAGTCAAGCTTACATCAGACTTCGACAACCCAAG--ATGGA
score      _000:ATG          C    CTC        TA A  AGAC  C ACAAC  AAG  AT GA
bolinopsin_000:ATG-------C----CTC---------TAGACGAGAC--CAACAACGAAAGCTATAGA


aequorin   _060:TTGGACGACACAAGCATATGT-TCAATTCC---TTGATGTCAACCAC---AAT-GGAAA
score      _060: TGG  G  A AAG  T  GT  C ATT  C    TTGATGTC A  AC   AT     AAA
bolinopsin_060:-TGGCTG--AGAAGTGTGGGTAACGATTGGCAGTTTGATGTCGAGGACGTTCATCCTAAA


aequorin   _120:AATCT------CTCTTGACGAGATGGTCTACA-AGGC-ATCT-GATATTGTC-ATC-AA
score      _120: A CT        CTCT  A GAGAT  TC ACA    C  ATCT GA A TG C  TC   A
bolinopsin_120:CAGCTTAGTCGGCTCTACAAGAGAT--TCGACACCTTCGATCTAGACAGTGACGGTCGTA
```

Fig. 6 continued

```
aequorin   _180:TAACCTTGGAGCAACA-CCTGAGCAAGCCAAACGACACAAAGA--TGCTGTAGAAGCCT
score      _180:T   C TGGA C A A CCTG  C  GCC   CGACA AA GA   GCTG  GAA   CT
bolinopsin_180:TGGACATGGA-CGAGATCCTGTACTGGCC---CGACAGAATGAGGCAGCTGGTGAACGCT

aequorin   _240:TCTTCGGAGGAGCTGGAATGAAATATGGTGTGGAAACTGATTG---GCCTGCAT--ATA
score      _240:TCT  GA AG T GA  GAA   G TG GG  CTG TTG     CCT C T  A A
bolinopsin_240:TCTGACGAACAGGTCGA--GAA----GATGAGG--GCTGCTTGCTACACCTTCTTCCACA

aequorin   _300:TTGAAGGA-TGGA---A-AAAATTGGCTACT----GATGAAT--TGGAG---AA-----
score      _300:    AAGGA TGGA   A AAAA G CT CT   GA GA T  T GAG   AA
bolinopsin_300:ACAAAGGAGTGGATCCAGAAAAGGACTCCTCAGAGAGACGACTGGGTTGAGGCTAACAGAG
```

Fig. 6 continued

```
aequorin   _360: -AT-----ACGCCAAAA-----ACGAACCAACG--------CTC----ATCCGTATAT
score      _360: AT    A GC AAA   A G A C ACG          CTC    AT GT T T
bolinopsin_360: TATTTGCTGAGGCTGAAAGAGAGAGGGAACGACGTGGCATGCCCTCCTTGATTGGTCTTT

aequorin   _420: GGGGTGATGCTTTGTTTGATATCGTTGACAAAGATCAAAATGGAGCCATTACACTGGATG
score      _420: G   GA GCTT  T  GAT TC T GA  A GA    ATGG  C TT   T GATG
bolinopsin_420: TGTCAGACGCTTACTACGATGTCCTGGATGATGACGGTGATGGTACTGTTGATGTTGATG

aequorin   _480: AA-TGGAAAGCATACACCAAAGCTGCTGGTATCATCCAATCATCAGAAGATTGGGAGGAA
score      _480: AA T AAA CAT A AA GCT TG AT  CC  C CAG AG T G   A
bolinopsin_480: AACTCAAAACCAT-GATGAAGGCTTTTG--ATGTGCC----C--CAGGAGGCT--GCCTAC
```

Fig. 6 continued

```
aequorin   _540:ACATTC---AGAGTGTGC-GATATTGATGAAAGTGGACAACTCGATGTTGATGAGATGAC
score      _540:AC TTC   A AG    GC GA A  GAT A AGTGGA AACT GA G  GA G GA  AC
bolinopsin_540:ACCTTCTTTA-AGAAAGCTGACACGGATAATAGTGGAAAACTGGA-G-AGAAGCGA--AC

aequorin   _600:AAGACAAACAT---TT-AGGA--TTTTGG-T--ACACCATGGATCCTGCTTGCGAAAAGCT
score      _600:  G C CAT  TT AG A  TT TGG T A CC    GATCCT   TG GA     T
bolinopsin_600:TGGTC--CATCTCTTCAGAAAGTTCTGGATGGAATCCTACGATCCTCAGTGGGACGGTGT

aequorin   _660:CTACG-GTGGAGCTGTCCCCTAA
score      _660:CTACG T A TT   TAA
bolinopsin_660:CTACGCTTACAAATAT----TAA
```

Fig. 7

```
AEQUORIN   _000:VKLTP-DFDNPKW---IG-------RH-KHM-----FNFLDVNHNGRISLDEMVYKA
score      _000: L|  || |W   |G     H K||    F |D| | GR| |DE||Y|
BOLINOPSIN_000:MPLDETNNESYRWLRSVGNDWQFDVEDVHPKQLSRLYKRFDTFDLDSDGRMDEILYWP

AEQUORIN   _060:SDIVINNLGATPEQAKRHKDAVEAFFGGAAMKYGVETEWPEYIEGW----KRLASEELKR
score      _060: D  || A |EQ||||||A| FF  | GV| E| | |W  | |A E |R
BOLINOPSIN_060:-DRMRQLVNASDEQVEKMRAACYTFF----HNKGVDPEKGLLRDDWVEANRVFAEAERER

AEQUORIN   _120:YSKNQITLIRLWGDALFDIIDKDQNGAISLDEWKAYTKSAGIIQSSEDCEETFRVCDIDE
score      _120: |   LI L DA||D| D D G  ||DE K |K| |Q E| F| D|D
BOLINOPSIN_120:ERRGMPSLIGLLSDAYDVLDDDGDGTVDVDELKTMMKAFDVPQ--EAAYTFFKKADTDN
```
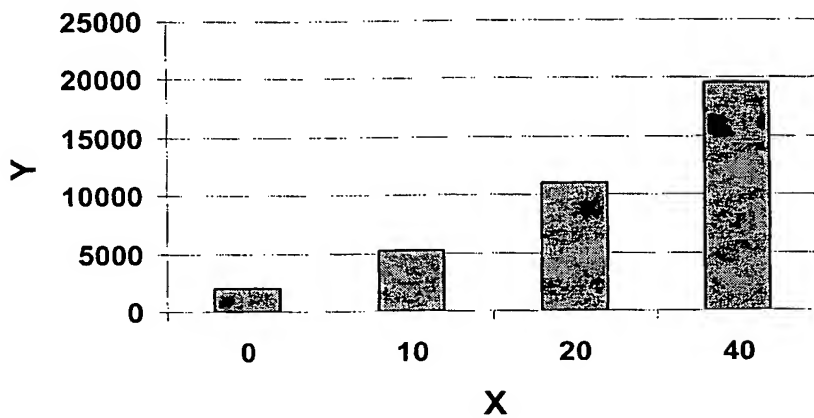
Fig. 7 continued

```
AEQUORIN    _180:SGQLDVDEMTRQHLG--FWY-TMDPACEKLYGGAV---P

score       _180:SG|L| E|   HL  FW|  |DP    |G||

BOLINOPSIN_180:SGKLERSEL--VHLFRKFWMESYDP----QWDGVYAYKY
```

Fig. 8

Fig. 9